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(54) Title: HAPLOTYPE PARTITIONING

(57) Abstract: The invention relates to a method for identifying mutations and/or polymorphisms that are major determinants of a selected phenotype and is based on the identification of haplotypes and the partitioning thereof into groups that are major determinants for said phenotype.

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INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER
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B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, MEDLINE, EMBASE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	CHASMAN D ET AL: "Predicting the functional consequences of non-synonymous single nucleotide polymorphisms: structure-based assessment of amino acid variation" JOURNAL OF MOLECULAR BIOLOGY, LONDON, GB, vol. 307, no. 2, 23 March 2001 (2001-03-23), pages 683-706, XP004466046 ISSN: 0022-2836 page 683 -page 690 page 694 -page 705 --- -/--	1-8

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Int. Patent Application No.

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

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